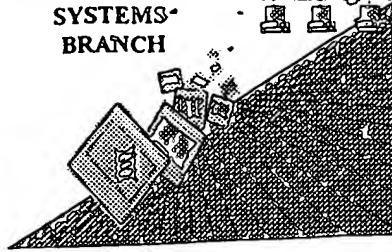


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/972916
Source: DF PLE
Date Processed by STIC: 10/19/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/972916</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENCLISII "ALPIIA" HEADERS, WHICH WERE INSERTED BY P1		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino <input type="checkbox"/> Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>..<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	A "bug" in PatentIn version 2.0 has caused the <220>..<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>..<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>..<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID.NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
9 <input type="checkbox"/> Use of n's or Xaa's <input type="checkbox"/> (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Invalid <213> <input type="checkbox"/> Response	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>..<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents	
11 <input type="checkbox"/> Use of <220>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>..<223> section is required when <213> response is Unknown or Artificial Sequence	
12 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
13 <input type="checkbox"/> Misuse of n	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	

Does Not Comply
Corrected Diskette Needed

* Does Not Comply
Corrected Diskette Needed

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Current Application date is 10-10-01
It is required that new format and
new rules are adhered to ~~not~~ a
mixture of both old and new format and
rules.

MMA

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/972,916

 DATE: 10/19/2001
 TIME: 10:48:35

Input Set: I972916.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

1 <110> APPLICANT: Thul, Peter M.
 2 <120> TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
 3 <130> FILE REFERENCE: US 1292/01 (VA)
 4 <140> CURRENT APPLICATION NUMBER: US/09/972,916 *(Emmended)*
 5 <141> CURRENT FILING DATE: 2001-10-10
 W--> 6 <150> EARLIER APPLICATION NUMBER
 7 <151> EARLIER FILING DATE: *These fields are mandatory if you wish to claim prior property rights. MA*
 8 <160> NUMBER OF SEQ ID NOS: 6
 9 <210> SEQ ID NO 1
 10 <211> LENGTH: 51
 11 <212> TYPE: DNA
 12 <213> ORGANISM: Rattus norvegicus
 13 <220> FEATURE:
 14 <221> NAME/KEY:
 15 <222> LOCATION:
 16 <223> OTHER INFORMATION: STRANDEDNESS: double
 17 TOPOLOGY: linear
 18 <400> SEQUENCE: SEQ ID NO: 1
 19 catggcgca cggggcactc ccgtggttcc tggactctgg cccccagtgt a *OR If you wish to use old Format. Does Not Comply and Corrected Diskette Needed* 51
 20 <210> SEQ ID NO 2
 21 <211> LENGTH: 219
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Rattus norvegicus
 24 <220> FEATURE:
 25 <221> NAME/KEY:
 26 <222> LOCATION:
 27 <223> OTHER INFORMATION: STRANDEDNESS: double
 28 TOPOLOGY: linear
 29 <400> SEQUENCE: SEQ ID NO: 2
 30 tcacaagcaa aacaaactta ttttgaacac ggggatccta gcacgctgcc ctgacaatca 60
 31 ttaaccgtg ctggcgagcc agcccttcat aaggccctgg gtatggccag ccagcatgg 120
 32 ccactgccc cccgagacaca aaccaggcga gcattgaaca ctgcacacgg ccatctgccc 180
 33 agagagctgt gaccaccact tccgctacta gctagccgc 219
 34 <210> SEQ ID NO 3
 35 <211> LENGTH: 270
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence *Does Not Comply and Corrected Diskette Needed*
 38 <220> FEATURE:
 39 <221> NAME/KEY:
 40 <222> LOCATION:
 41 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA *Erroneous*
 42 STRANDEDNESS: double
 43 TOPOLOGY: both *choose new format*
 44 <400> SEQUENCE: SEQ ID NO: 3 *Emmended*

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/972,916

 DATE: 10/19/2001
 TIME: 10:48:35

Input Set: I972916.RAW

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47      gctgccgagc cagcccttca taaggccctg ggtatggcca gccagcatgg tccactgccc 180
48      gccgagacac aaacccagcg agcattgaac actgcacacg gccatctgcc cagagagctg 240
49      tgaccaccac ttccgctact agctagccgc 270

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53 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <221> NAME/KEY:
56 <222> LOCATION:
57 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA
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59     TOPOLOGY: both
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63     tattttgaac acggggatcc tagcacgctg ccctgacaat cattaaccgg tgctg(ccag 180
64     ccagcccttc ataaggccct gggtatggcc agccagcatg gtccactgccc cgccgagaca 240
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72 <221> NAME/KEY:
73 <222> LOCATION:
74 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA
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76     TOPOLOGY: both
77 <400> SEQUENCE: SEQ ID NO: 5
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80     ccaggaacca cgggagtgc(cc ccgtgc(ccc atgtcacaag caaaaacaaac ttatttgaa 180
81     cacggggatc ctagcacgct gcctgacaat cattaaccgg tgctg(cca gccagccctt 240
82     cataaggccc tgggtatggc cagccagcat ggtccactgccc ccgccgagac acaaaccac 300
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84     cttagctagcc gc 372

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87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE: Errored
90 <221> NAME/KEY:
91 <222> LOCATION:
92 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DNA
93     STRANDEDNESS: double
94     TOPOLOGY: both

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PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/972,916DATE: 10/19/2001
TIME: 10:48:35

Input Set: I972916.RAW

95 <400> SEQUENCE: SEQ ID NO: 6
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98 tcccgtggtt cctggactct ggccccagt gtacatggc gcacggggca ctcccgtgg 180
99 tcctggactc tggcccccag tgtatcacaa gcaaaacaaa cttatggta acacggggat 240
100 ccttagcacgc tgccctgaca atcatggacc cgtgctgccc agccagccct tcataaggcc 300
101 ctgggtatgg ccagccagca tggtccactg cccgcccaga cacaaccca gcgagcattg 360
102 aacactgcac acggccatct gcccagagag ctgtgaccac cactccgct actagctagc 420
103 cgc 423

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